In the Specification

Please replace the title at page 1, line 1 with the following title:

- - -METHODS OF IDENTIFYING POINT MUTATIONS IN A GENOME THAT CAUSE OR ACCELERATE DISEASE- - -

Amendments to the specification are indicated in the attached "Marked Up Version of Amendments" (page i).

In the Claims

Please amend Claims 25 and 33. Amendments to the claims are indicated in the attached "Marked Up Version of Amendments" (pages i - ii).

25. (Amended) A method for identifying genes which carry a harmful allele, comprising:

a) identifying the inherited point mutations which are found in the genes or portions thereof of a population of young individuals, wherein the set of all inherited point mutations occurring at a frequency at about or above 5×10^{-5} can be identified, and determining the frequencies with which each point mutation occurs;

b) identifying the set of inherited point mutations which are found in the genes or portions thereof of a population of aged individuals, and determining the frequency with which each point mutation occurs; and

c) comparing the frequency of each point mutation identified in a selected gene or portion thereof of the young population determined in a) with the frequency of the same point mutations identified in said selected gene of the aged population determined in b), wherein a significant decrease in the frequency of two or more point mutations in said selected gene of the aged population relative to said selected gene of the young population indicates that said selected gene carries a harmful allele.